



RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: 09/762224
Source: PCT09
Date Processed by STIC: 09/24/01

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,224

DATE: 09/24/2001

TIME: 15:58:37

Input Set : A:\Seq List-Pur-115.txt

Output Set: N:\CRF3\09242001\I762224.raw

W--> 1 PUR-115:JJS:133252

5 <110> APPLICANT: Sanders, David A.

6 Kuhn, Richard John

7 Jeffers, Scott A.

8 Sharkey, Curtis Matthew

9 North, Cynthia Lin

10 Fishbach, Michael A.

12 <120> TITLE OF INVENTION: PSEUDOTYPED RETROVIRUSES AND STABLE CELL LINES FOR THEIR PRODUCTION

14 <130> FILE REFERENCE: 7024-497/PUR-115

16 <140> CURRENT APPLICATION NUMBER: US 09/762,224

18 <141> CURRENT FILING DATE: 2001-02-02

20 <150> PRIOR APPLICATION NUMBER: PCT/US99/17702

22 <151> PRIOR FILING DATE: 1999-08-04

24 <150> PRIOR APPLICATION NUMBER: U.S. 60/095,242

26 <151> PRIOR FILING DATE: 1998-08-04

28 <150> PRIOR APPLICATION NUMBER: U.S. 60/112,405

30 <151> PRIOR FILING DATE: 1998-12-15

32 <160> NUMBER OF SEQ ID NOS: 3

34 <170> SOFTWARE: Microsoft Word 97

Does Not Comply
Corrected Diskette Needed*Errored:
Field 211 indicates 2176
nucleotides. Found 2224.*

ERRORED SEQUENCES

*Errored from line 372 - integer end total indicates
757 nucleotides. There are 727 nucleotides at
the end of line 368 and 48 nucleotides on line 759.
48 + 727 = 775 ≠ 757 There's your
end total is 2176 + 48 = 2224 nucleotides*

301 <210> SEQ ID NO: 2
 303 <211> LENGTH: 2176
 305 <212> TYPE: DNA
 307 <213> ORGANISM: Filovirus Ebola virus, subtype Zaire
 309 <400> SEQUENCE: 2

312	caacaacaca atg ggc gtt aca gga ata ttg cag tta cct cgt gat cga ttc aag	55
313	Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys	
314	1 5 10 15	
316	agg aca tca ttc ttt ctt tgg gta att atc ctt ttc caa aga aca ttt	103
317	Arg Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe	
318	20 25 30	
320	tcc atc cca ctt gga gtc atc cac aat agc aca tta cag gtt agt gat	151
321	Ser Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp	
322	35 40 45	
324	gtc gac aaa cta gtt tgt cgt gac aaa ctg tca tcc aca aat caa ttg	199
325	Val Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu	
326	50 55 60	
328	aga tca gtt gga ctg aat ctc gaa ggg aat gga gtg gca act gac gtg	247
329	Arg Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val	
330	65 70 75	
332	cca tct gca act aaa aga tgg ggc ttc agg tcc ggt gtc cca cca aag	295
333	Pro Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys	
334	80 85 90 95	
336	gtg gtc aat tat gaa gct ggt gaa tgg gct gaa aac tgc tac aat ctt	343

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337	Val	Val	Asn	Tyr	Glu	Ala	Gly	Glu	Trp	Ala	Glu	Asn	Cys	Tyr	Asn	Leu		
338					100					105					110			
340	gaa	atc	aaa	aaa	cct	gac	ggg	agt	gag	tgt	cta	cca	gca	gcg	cca	gac	391	
341	Glu	Ile	Lys	Lys	Pro	Asp	Gly	Ser	Glu	Cys	Leu	Pro	Ala	Ala	Pro	Asp		
342					115					120					125			
344	ggg	att	cgg	ggc	ttc	ccc	cgg	tgc	cgg	tat	gtg	cac	aaa	gta	tca	gga	439	
345	Gly	Ile	Arg	Gly	Phe	Pro	Arg	Cys	Arg	Tyr	Val	His	Lys	Val	Ser	Gly		
346					130					135					140			
348	acg	gga	ccg	tgt	gcc	gga	gac	ttt	gcc	ttc	cat	aaa	gag	ggt	gct	ttc	487	
349	Thr	Gly	Pro	Cys	Ala	Gly	Asp	Phe	Ala	Phe	His	Lys	Glu	Gly	Ala	Phe		
350					145					150					155			
352	ttc	ctg	tat	gat	cga	ctt	gct	tcc	aca	gtt	atc	tac	cga	gga	acg	act	535	
353	Phe	Leu	Tyr	Asp	Arg	Leu	Ala	Ser	Thr	Val	Ile	Tyr	Arg	Gly	Thr	Thr		
354	160					165					170				175			
356	ttc	gct	gaa	ggt	gtc	gtt	gca	ttt	ctg	ata	ctg	ccc	caa	gct	aag	aag	583	
357	Phe	Ala	Glu	Gly	Val	Val	Ala	Phe	Leu	Ile	Leu	Pro	Gln	Ala	Lys	Lys		
358					180						185				190			
360	gac	ttc	ttc	agc	tca	cac	ccc	ttg	aga	gag	ccg	gtc	aat	gca	acg	gag	631	
361	Asp	Phe	Phe	Ser	Ser	His	Pro	Leu	Arg	Glu	Pro	Val	Asn	Ala	Thr	Glu		
362					195					200					205			
364	gac	ccg	tct	agt	ggc	tac	tat	tct	acc	aca	att	aga	tat	cag	gct	acc	679	
365	Asp	Pro	Ser	Ser	Gly	Tyr	Tyr	Ser	Thr	Thr	Ile	Arg	Tyr	Gln	Ala	Thr		
366					210					215					220			
368	ggt	ttt	gga	acc	aat	gag	aca	gag	tac	ttg	ttc	gag	gtt	gac	aat	ttg	727	
369	Gly	Phe	Gly	Thr	Asn	Glu	Thr	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Asn	Leu	+48	
370					225					230					235		757	
E-->	372	acc	tac	gtc	caa	ctt	gaa	tca	aga	ttc	aca	cca	cag	ttt	ctg	ctc	cag	
	373	Thr	Tyr	Val	Gln	Leu	Glu	Ser	Arg	Phe	Thr	Pro	Gln	Phe	Leu	Leu	Gln	
	374	240					245					250				255		
E-->	376	ctg	aat	gag	aca	ata	tat	aca	agt	ggg	aaa	agg	agc	aat	acc	acg	gga	775
	377	Leu	Asn	Glu	Thr	Ile	Tyr	Thr	Ser	Gly	Lys	Arg	Ser	Asn	Thr	Thr	Gly	
	378					260					265				270			
E-->	380	aaa	cta	att	tgg	aag	gtc	aac	ccc	gaa	att	gat	aca	aca	atc	ggg	gag	823
	381	Lys	Leu	Ile	Trp	Lys	Val	Asn	Pro	Glu	Ile	Asp	Thr	Thr	Ile	Gly	Glu	
	382					275					280				285			
E-->	384	tgg	gcc	ttc	tgg	gaa	act	aaa	aaa	aac	ctc	act	aga	aaa	att	cgc	agt	871
	385	Trp	Ala	Phe	Trp	Glu	Thr	Lys	Lys	Asn	Leu	Thr	Arg	Lys	Ile	Arg	Ser	
	386					290				295					300			
E-->	388	gaa	gag	ttg	tct	ttc	aca	gtt	gta	tca	aac	gga	gcc	aaa	aac	atc	agt	919
	389	Glu	Glu	Leu	Ser	Phe	Thr	Val	Val	Ser	Asn	Gly	Ala	Lys	Asn	Ile	Ser	
	390					305				310					315			
E-->	392	ggt	cag	agt	ccg	gcg	cga	act	tct	tcc	gac	cca	ggg	acc	aac	aca	aca	967
	393	Gly	Gln	Ser	Pro	Ala	Arg	Thr	Ser	Ser	Asp	Pro	Gly	Thr	Asn	Thr	Thr	
	394	320					325				330				335			
E-->	396	act	gaa	gac	cac	aaa	atc	atg	gct	tca	gaa	aat	tcc	tct	gca	atg	gtt	1015
	397	Thr	Glu	Asp	His	Lys	Ile	Met	Ala	Ser	Glu	Asn	Ser	Ser	Ala	Met	Val	
	398					340					345				350			
E-->	400	caa	gtg	cac	agt	caa	gga	agg	gaa	gct	gca	gtg	tcg	cat	cta	aca	acc	1063
	401	Gln	Val	His	Ser	Gln	Gly	Arg	Glu	Ala	Ala	Val	Ser	His	Leu	Thr	Thr	

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```

      402          355          360          365
E--> 404 ctt gcc aca atc tcc acg agt ccc caa tcc ctc aca acc aaa cca ggt      1111
      405 Leu Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly
      406          370          375          380
E--> 408 ccg gac aac agc acc cat aat aca ccc gtg tat aaa ctt gac atc tct      1159
      409 Pro Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser
      410          385          390          395
E--> 412 gag gca act caa gtt gaa caa cat cac cgc aga aca gac aac gac agc      1207
      413 Glu Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser
      414 400          405          410          415
E--> 416 aca gcc tcc gac act ccc tct gcc acg acc gca gcc gga ccc cca aaa      1255
      417 Thr Ala Ser Asp Thr Pro Ser Ala Thr Thr Ala Ala Gly Pro Pro Lys
      418          420          425          430
E--> 420 gca gag aac acc aac acg agc aag agc act gac ttc ctg gac ccc gcc      1303
      421 Ala Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp Pro Ala
      422          435          440          445
E--> 424 acc aca aca agt ccc caa aac cac agc gag acc gct ggc aac aac aac      1351
      425 Thr Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn
      426          450          455          460
E--> 428 act cat cac caa gat acc gga gaa gag agt gcc agc agc ggg aag cta      1399
      429 Thr His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu
      430          465          470          475
E--> 432 ggc tta att acc aat act att gct gga gtc gca gga ctg atc aca ggc      1447
      433 Gly Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly
W--> 434 485          490          495          500
E--> 436 ggg aga aga act cga aga gaa gca att gtc aat gct caa ccc aaa tgc      1495
      437 Gly Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys
W--> 438          505          510          515
E--> 440 aac cct aat tta cat tac tgg act act cag gat gaa ggt gct gca atc      1543
      441 Asn Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile
W--> 442          520          525          530
E--> 444 gga ctg gcc tgg ata cca tat ttc ggg cca gca gcc gag gga att tac      1591
      445 Gly Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr
W--> 446          535          540          545
E--> 448 ata gag ggg cta atg cac aat caa gat ggt tta atc tgt ggg ttg aga      1639
      449 Ile Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg
W--> 450          550          555          560
E--> 452 cag ctg gcc aac gag acg act caa gct ctt caa ctg ttc ctg aga gcc      1687
      453 Gln Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala
W--> 454 565          570          575          580
E--> 456 aca act gag cta cgc acc ttt tca atc ctc aac cgt aag gca att gat      1735
      457 Thr Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp
W--> 458          585          590          595
E--> 460 ttc ttg ctg cag cga tgg ggc ggc aca tgc cac att ctg gga ccg gac      1783
      461 Phe Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp
W--> 462          600          605          610
E--> 464 tgc tgt atc gaa cca cat gat tgg acc aag aac ata aca gac aaa att      1831
      465 Cys Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile
W--> 466          615          620          625

```

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```

E--> 468 gat cag att att cat gat ttt gtt gat aaa acc ctt ccg gac cag ggg      1879
      469 Asp Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly
W--> 470      630                      635                      640
E--> 472 gac aat gac aat tgg tgg aca gga tgg aga caa tgg ata ccg gca ggt      1927
      473 Asp Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly
W--> 474 645                      650                      655                      660
E--> 476 att gga gtt aca ggc gtt ata att gca gtt atc gct tta ttc tgt ata      1975
      477 Ile Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile
W--> 478                      665                      670                      675
E--> 480 tgc aaa ttt gtc ttt tag tttttcttca gattgcttca tggaaaagct cagcctcaaa    2033
      481 Cys Lys Phe Val Phe
W--> 482                      680
E--> 484 tcaatgaaac caggatttaa ttatatggat tacttgaatc taagattact tgacaaatga    2093
E--> 486 taatataata cactggagct ttaaacaatag ccaatgtgat tctaactcct ttaaactcac    2153
E--> 488 agttaatcat aaacaagggtt tga                                          2176

```

VERIFICATION SUMMARY

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Input Set : A:\Seq List-Pur-115.txt

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L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:372 M:254 E: No. of Bases conflict, LENGTH:Input:757 Counted:775 SEQ:2
M:254 Repeated in SeqNo=2
L:384 M:112 C: (48) String data converted to lower case,
L:434 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:488 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2176 Found:2224 SEQ:2
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:548 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:552 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:568 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:576 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:584 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:588 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:592 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:596 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:600 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:604 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:608 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:612 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:616 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:620 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:624 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:628 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:632 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:636 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:640 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:648 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:652 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:656 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:660 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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L:664 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

L:668 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

L:672 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3